

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2008; month=4; day=25; hr=14; min=3; sec=3; ms=423;]

=====

Application No: 10539962

Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-14 16:27:59.858

Finished: 2008-04-14 16:28:01.311

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 453 ms

Total Warnings: 20

Total Errors: 0

No. of SeqIDs Defined: 37

Actual SeqID Count: 37

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)

Input Set:

Output Set:

Started: 2008-04-14 16:27:59.858
Finished: 2008-04-14 16:28:01.311
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 453 ms
Total Warnings: 20
Total Errors: 0
No. of SeqIDs Defined: 37
Actual SeqID Count: 37

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> FAGAN, RICHARD JOSEPH
 PHELPS, CHRISTOPHER BENJAMIN
 RODRIGUES, TANIA MARIA
 POWER, CHRISTINE
 DE TIANI, MARIATELLA

<120> SPLICE VARIANT OF HUMAN PLACENTAL GROWTH HORMONE

<130> C&R-106

<140> 10539962

<141> 2008-04-14

<150> PCT/GB03/05594

<151> 2003-12-19

<150> GB 0229850.3

<151> 2002-12-20

<160> 37

<170> SeqWin99, version 1.02

<210> 1

<211> 180

<212> DNA

<213> Homo sapiens

<400> 1

gctcccgac	gctccctgctc	ctggettttg	gcctgetctg	cctgtcctgg	cttcaagagg	60
gcagtgcctt	cccaaccatt	cccttatcca	ggctttttga	caacgctatg	ctccgcgccc	120
gtcgcctgta	ccagctggca	tatgacacct	atcaggagtt	tgtaagctct	tgggtaatgg	180

<210> 2

<211> 60

<212> PRT

<213> Homo sapiens

<400> 2

Ser	Arg	Thr	Ser	Leu	Leu	Leu	Ala	Phe	Gly	Leu	Leu	Cys	Leu	Ser	Trp
1			5				10						15		

Leu	Gln	Glu	Gly	Ser	Ala	Phe	Pro	Thr	Ile	Pro	Leu	Ser	Arg	Leu	Phe
		20						25					30		

Asp	Asn	Ala	Met	Leu	Arg	Ala	Arg	Arg	Leu	Tyr	Gln	Leu	Ala	Tyr	Asp
		35					40					45			

Thr	Tyr	Gln	Glu	Phe	Val	Ser	Ser	Trp	Val	Met	Glu
	50					55					60

<210> 3

<211> 47

<212> DNA

<213> Homo sapiens

<400> 3

agtctattcc aacaccttcc aacaggggtga aaacgcagca gaaatct 47

<210> 4

<211> 15

<212> PRT

<213> Homo sapiens

<400> 4

Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser
1 5 10 15

<210> 5

<211> 227

<212> DNA

<213> Homo sapiens

<400> 5

gctcccgac gtcctgctc ctggcttttg gctgctctg cctgtcctgg cttcaagagg 60
gcagtgcctt cccaaccatt cccttatcca ggctttttga caacgctatg ctccgcgccc 120
gtcgctgta ccagctggca tatgacacct atcaggagtt tgtaagctct tgggtaatgg 180
agtctattcc aacaccttcc aacaggggtga aaacgcagca gaaatct 227

<210> 6

<211> 75

<212> PRT

<213> Homo sapiens

<400> 6

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Ser Trp
1 5 10 15

Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe
20 25 30

Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp
35 40 45

Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu Ser Ile Pro Thr
50 55 60

Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser
65 70 75

<210> 7

<211> 600

<212> DNA

<213> Homo sapiens

<400> 7

atggctgcag gctcccgac gtcctgctc ctggcttttg gctgctctg cctgtcctgg 60
cttcaagagg gcagtgcctt cccaaccatt cccttatcca ggctttttga caacgctatg 120
ctccgcgccc gtcgctgta ccagctggca tatgacacct atcaggagtt tgtaagctct 180
tgggtaatgg agtctattcc aacaccttcc aacaggggtga aaacgcagca gaaatctaac 240
ctagagctgc tccgcatctc cctgctgctc atccagtcac ggctggagcc cgtgcagctc 300

```

ctcaggagcg ttttcgccaa cagcctgggtg tatggcgccct cggacagcaa cgtctatcgc 360
cacctgaagg acctagagga aggcattccaa acgctgatgt ggaggctgga agatggcagc 420
ccccggactg ggcagatctt caatcagtcc tacagcaagt ttgacacaaa atcgcacaaac 480
gatgacgcac tgctcaagaa ctacgggctg ctctactgct tcaggaagga catggacaag 540
gtcgagacat tcttgcgcac cgtgcagtgc cgctctgtgg agggcagctg tggcttctag 600

```

```

<210> 8
<211> 199
<212> PRT
<213> Homo sapiens

```

```

<400> 8
Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

```

```

Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

```

```

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln
35 40 45

```

```

Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu
50 55 60

```

```

Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn
65 70 75 80

```

```

Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu
85 90 95

```

```

Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly
100 105 110

```

```

Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly
115 120 125

```

```

Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly
130 135 140

```

```

Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn
145 150 155 160

```

```

Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys
165 170 175

```

```

Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser
180 185 190

```

```

Val Glu Gly Ser Cys Gly Phe
195

```

```

<210> 9
<211> 522
<212> DNA
<213> Homo sapiens

```

```

<400> 9

```

ttcccaacca	ttcccttata	caggtttttt	gacaacgcta	tgctccgcgc	cgtcgcttg	60
taccagctgg	catatgacac	ctatcaggag	tttgtaagct	cttgggtaat	ggagtctatt	120
ccaacacctt	ccaacagggt	gaaaacgcag	cagaaatcta	acctagagct	gctccgcata	180
tccttgctgc	tcattccagtc	atggctggag	cccgtgcagc	tcctcaggag	cgtcttcgcc	240
aacagcctgg	tgtatggcgc	ctcggacagc	aacgtctata	gccacctgaa	ggacctagag	300
gaaggcatcc	aaacgctgat	gtggaggctg	gaagatggca	gccccggac	tgggcagatc	360
ttcaatcagt	cctacagcaa	gtttgacaca	aaatcgca	acgatgacgc	actgctcaag	420
aactacgggc	tgctctactg	cttcaggaag	gacatggaca	aggtcgagac	attcctgcgc	480
atcgtgcagt	gccgctctgt	ggagggcagc	tgtggcttct	ag		522

<210> 10
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 10
 Phe Pro Thr Ile Pro Leu Ser Arg Leu Phe Asp Asn Ala Met Leu Arg
 1 5 10 15
 Ala Arg Arg Leu Tyr Gln Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val
 20 25 30
 Ser Ser Trp Val Met Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys
 35 40 45
 Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu
 50 55 60
 Ile Gln Ser Trp Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala
 65 70 75 80
 Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu
 85 90 95
 Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp
 100 105 110
 Gly Ser Pro Arg Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe
 115 120 125
 Asp Thr Lys Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu
 130 135 140
 Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg
 145 150 155 160
 Ile Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe
 165 170

<210> 11
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer GCP Forward

<400> 11
 ggggacaagt ttgtacaaaa aagcaggctt cgccacc 37

<210> 12
 <211> 51
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer GCP Reverse

<400> 12
 ggggaccact ttgtacaaga aagctggggt tcaatgggtga tggatgatggt g 51

<210> 13
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer INSP105-exon2F

<400> 13
 gcaggcttcg ccaccatggc tgcaggctcc cggacgtccc tgetcctg 48

<210> 14
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer INSP105-exon2R

<400> 14
 ggaaggtggt ggaatagact ccattaccca agagctta 38

<210> 15
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer INSP105- exon3F

<400> 15
 agctcttggg taatggagtc tattccaaca ccttcc 36

<210> 16
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer INSP105- exon3R

<400> 16
 ggagcagctc taggttagat ttctgctgcg ttttca 36

<210> 17
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105- exon4F

 <400> 17
 aacgcagcag aaatctaacc tagagctgct ccgcac 37

 <210> 18
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105- exon4R

 <400> 18
 tgccatcttc cagcctccac atcagcggtt ggatgc 36

 <210> 19
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105- exon5F

 <400> 19
 ccaaacgtg atgtggaggc tggaagatgg cagccc 36

 <210> 20
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105- exon5R

 <400> 20
 gtgatggtga tgggtggaagc cacagctgcc ctcca 35

 <210> 21
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105-5' end-R

 <400> 21
 ggtagattt ctgctgcgtt ttcaccctgt tg 32

 <210> 22

<211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105-center-F

 <400> 22
 caacagggtg aaaacgcagc agaaatctaa cc 32

 <210> 23
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105-center-R

 <400> 23
 ggctgccatc ttccagcctc ca 22

 <210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer INSP105-3' end-F

 <400> 24
 gcatccaaac gctgatgtgg ag 22

 <210> 25
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer pEAK12-F

 <400> 25
 gccagcttgg cacttgatgt 20

 <210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer pEAK12-R

 <400> 26
 gatggaggtg gacgtgtcag 20

 <210> 27
 <211> 18
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer M13F

<400> 27

caggaaacag ctatgacc 18

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer M13R

<400> 28

tgtaaaacga cggccagt 18

<210> 29

<211> 129

<212> DNA

<213> Homo sapiens

<400> 29

tccttgcctgc tcatccagtc atggctggag cccgtgcagc tcttcaggag cgtcttcgcc 60
aacagcctgg tgtatggcgc ctcggacagc aacgtctatc gccacctgaa ggacctagag 120
gaaggcatc 129

<210> 30

<211> 217

<212> PRT

<213> Homo sapiens

<400> 30

Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln
35 40 45

Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Leu Lys
50 55 60

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65 70 75 80

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys
85 90 95

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100 105 110

Leu Glu Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val
115 120 125

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu
130 135 140

Glu Gly Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg
145 150 155 160

Thr Gly Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser
165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
210 215

<210> 31
<211> 597
<212> DNA
<213> Homo sapiens

<220>
<221> Exon
<222> (1)..(597)

<400> 31
atg gct gca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc 48
Met Ala Ala Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

tgc ctg tcc tgg ctt caa gag ggc agt gcc ttc cca acc att ccc tta 96
Cys Leu Ser Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20 25 30

tcc agg ctt ttt gac aac gct atg ctc cgc gcc cgt cgc ctg tac cag 144
Ser Arg Leu Phe Asp Asn Ala Met Leu Arg Ala Arg Arg Leu Tyr Gln

35	40	45	
ctg gca tat gac acc tat cag gag ttt gta agc tct tgg gta atg gag			192
Leu Ala Tyr Asp Thr Tyr Gln Glu Phe Val Ser Ser Trp Val Met Glu			
50	55	60	
tct att cca aca cct tcc aac agg gtg aaa acg cag cag aaa tct aac			240
Ser Ile Pro Thr Pro Ser Asn Arg Val Lys Thr Gln Gln Lys Ser Asn			
65	70	75	80
cta gag ctg ctc cgc atc tcc ctg ctg ctc atc cag tca tgg ctg gag			288
Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp Leu Glu			
	85	90	95
ccc gtg cag ctc ctc agg agc gtc ttc gcc aac agc ctg gtg tat ggc			336
Pro Val Gln Leu Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly			
	100	105	110
gcc tcg gac agc aac gtc tat cgc cac ctg aag gac cta gag gaa ggc			384
Ala Ser Asp Ser Asn Val Tyr Arg His Leu Lys Asp Leu Glu Glu Gly			
	115	120	125
atc caa acg ctg atg tgg agg ctg gaa gat ggc agc ccc cgg act ggg			432
Ile Gln Thr Leu Met Trp Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly			
	130	135	140
cag atc ttc aat cag tcc tac agc aag ttt gac aca aaa tcg cac aac			480
Gln Ile Phe Asn Gln Ser Tyr Ser Lys Phe Asp Thr Lys Ser His Asn			
145	150	155	160
gat gac gca ctg ctc aag aac tac ggg ctg ctc tac tgc ttc agg aag			528
Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys			
	165	170	175
gac atg gac aag gtc gag aca ttc ctg cgc atc gtg cag tgc cgc tct			576
Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser			
	180	185	190
gtg gag ggc agc tgt ggc ttc			597
Val Glu Gly Ser Cys Gly Phe			
195			

<210> 32
 <211> 597
 <212> DNA
 <213> Homo sapiens

<400> 32	
ctggctgcag gctccggac gtcctgtc ctggttttg gctgtctg cctgtcctgg	60
cttcaagagg gcagtgcctt cccaaccatt cccttatcca ggctttttga caacgctatg	120
ctccgcgcc gtcgctgta ccagctggca tatgacacct atcaggagtt tgtaagctct	180
tgggtaatgg agtctattcc aacacctcc aacagggtga aaacgcagca gaaatctcac	240

ctagagctgc tccgcatctc cctgctgctc atcgagtcgt ggctggagcc cgtgcagttc	300
ctcaggagtg tcttcgccaa cagcctggtg tacggcgctt ctgacagcaa cgtctatgac	360
ctcctaaagg acctagagga aggcattcaa acgctgatgt ggaggctgga agatggcagc	420
ccccggactg ggcagatctt caagcagacc tacagcaagt ttgacacaaa ctgcacaaac	480
catgacgcac tgctcaagaa ctacgggctg ctccactgct tcaggaagga catggacaag	540
gtcgagacat tcttgccgat cgtgcagtgc cgtctctgtg agggcagctg tggcttc	597

<210> 33
 <211> 589
 <212> DNA
 <213> Homo sapiens

<400> 33	
atggctccgg acgtccctgc tcttggtttt tggcctgctc tgcttgcctt ggcttcaaga	60
gggcagtgcc ttcccaacca ttcccttatt caggcttttt gacaacgcta tgctccgcgc	120
ccatcgtctg caccagctgg cctttgacac ctaccaggag tttgtaagct cttgggtaat	180
ggagtctatt ccaacacctt ccaacagggt gaaaccgcag cagaaatcta acctagagct	240
gtcctcgcatc tccctgctgc tcatccagtc atggctggag cccgtgcagc tcttcaggag	300
cgtcttcgcc aacagcctgg tgtatggcgc ctccgacagc aacgtctatc gccacctgaa	360
ggacctagag gaaggcatcc aaacgctgat gtggaggctg gaagatggca gccacctgac	420
tgggcagacc ctcaagcaga cctacagcaa gtttgacaca aactcgcaca accatgacgc	480
actgctcaag aactacgggc tgctccactg cttcaggaag gacatggaca aggtcgagac	540
attcctgcgc atcgtgcagt gccgctctgt ggagggca	